

Day : Monday
Date: 10/18/2004

Time: 09:53:11

 **PALM INTRANET**

Biotech Query for 10/043539

Title: **COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE
DETERMINANTS IN BACTERIA**

Inventor: **CHEUNG, AMBROSE**

Location:

Location Date:

Group Art Unit: **1645**

Status: **71/RESPONSE TO NON-FINAL OFFICE ACTION ENTERED AND FORWARDED
TO EXAMINER**

Barcode: **10043539CA**

Num	Date	Code	Contents Description
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4	09/06/2002	CRFE	CRF IS GOOD TECHNICALLY / ENTERED INTO DATABASE

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☐ 2. [5976792](#). 08 Jul 96; 02 Nov 99. Regulation of exoprotein in staphylococcus aureus. Cheung; Ambrose, et al. 435/6; 435/320.1 530/350 530/387.1 530/388.1 530/388.4 530/825 536/23.7 536/24.32. C12Q001/68 C07H021/04 C12N015/74 C07K014/31 C07K016/12.

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L3: Entry 5 of 6

File: DWPI

Sep 6, 2002

DERWENT-ACC-NO: 2002-706985

DERWENT-WEEK: 200276

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TITLE: New sarR gene from the locus of Staphylococcus aureus, useful for treating gram-positive bacteremia

INVENTOR: CHEUNG, A L; MANNA, A ; ZHANG, G

PATENT-ASSIGNEE: DARTMOUTH COLLEGE (DARTN)

PRIORITY-DATA: 2001US-289601P (May 8, 2001), 2001US-261233P (January 12, 2001),
2001US-261607P (January 12, 2001)

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PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<input type="checkbox"/> <u>WO 200268610 A2</u>	September 6, 2002	E	062	C12N000/00

DESIGNATED-STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE
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LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN
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LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

APPLICATION-DATA:

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
WO 200268610A2	January 11, 2002	2002WO-US00877	

INT-CL (IPC): C12 N 0/00

ABSTRACTED-PUB-NO: WO 200268610A

BASIC-ABSTRACT:

NOVELTY - An isolated nucleic acid sequence (I), which regulates the expression of virulence determinants in gram-positive bacteria, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

- (1) a vector (II) comprising the nucleic acid sequence;
- (2) a host cell (III) comprising the vector;
- (3) a method (IV) for identifying putative agents that inhibit growth and infectivity of bacteria;

- (4) a method (V) of inhibiting growth and infectivity of bacteria;
- (5) a pharmaceutical composition (VI) for use as an anti-bacterial agent comprising the agent that enhances the expression of the nucleic acid sequence or the activity of the polypeptide that it encodes and a vehicle or the compound identified by the method of (X) or a compound that binds to the P1 promoter region of a sarA gene;
- (6) an isolated polypeptide (VII) that regulates the expression of virulence determinants in gram-positive bacteria;
- (7) a kit (VIII) for identifying the presence of a sarR gene or its product comprising a means for analyzing a biological sample for the presence of the sarR gene or its product;
- (8) a method (IX) of treating a mammal suffering from or susceptible to a gram-positive bacterial infection; or
- (9) a method (X) of screening for lead compounds that inhibit the expression of virulence determinants in gram-positive bacteria.

ACTIVITY - Antibacterial.

No biological data given.

MECHANISM OF ACTION - SarR-Agonist.

USE - The pharmaceutical composition comprising a sarR agonist or a compound capable of selective occupation of a sarA promoter receptor is useful for treating gram-positive bacteremia (claimed).

ABSTRACTED-PUB-NO: WO 200268610A
EQUIVALENT-ABSTRACTS:

CHOSEN-DRAWING: Dwg.0/12

DERWENT-CLASS: B04 D16
CPI-CODES: B04-C01; B04-E01; B04-E02F; B04-E03F; B04-E08; B04-F0100E; B04-F10B; B04-F10B0E; B04-F10B3; B04-F10B3E; B04-N03A0E; B11-A01; B11-C08E1; B11-C08F; B11-C08F2; B11-C08F4; B11-C08G; B11-C10; B12-K04E; B14-A01B; B14-A01B4; D05-H04; D05-H08; D05-H09; D05-H12A; D05-H12E; D05-H14; D05-H17A6; D05-H18;

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File: PGPB

Jul 3, 2003

PGPUB-DOCUMENT-NUMBER: 20030124597

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030124597 A1

TITLE: Compositions and methods for identifying agents which regulate autolytic processes in bacteria

PUBLICATION-DATE: July 3, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Cheung, Ambrose	Hanover	NH	US	

US-CL-CURRENT: 435/6; 435/227, 435/252.3, 435/320.1, 435/69.1, 514/12, 514/193, 514/200, 536/23.2

CLAIMS:

What is claimed is:

1. A nucleic acid sequence encoding a polypeptide which regulates expression of polypeptides involved in autolytic processes in bacteria.
2. The nucleic acid sequence of claim 1 wherein the bacteria is Staphylococcus aureus.
3. The nucleic acid of claim 1 wherein the bacteria comprises Staphylococcus, Sinorhizobium, Listeria, Clostridium, Bacillus, Corynebacterium, Brucella, Pseudomonas, Shweanella, Mesorhizobium, Caulobacter, Lactococcus, Mycobacterium, Burkholderia, Geobacter, Treponema, Vibrio, Escherichia, Enterococcus, Salmonella, Klebsiella, Agrobacterium, Yersinia, Bordetella, Actinobacillus, Streptomyces, Streptococcus, or Acinetobacter.
4. A nucleic acid sequence comprising SEQ ID NO: 1 or SEQ ID NO: 2.
5. A vector comprising the nucleic acid sequence of claim 1.
6. A host cell comprising the vector of claim 5.
7. A method for identifying agents that modulate autolysis in a bacterium comprising contacting a test cell, which contains a nucleic acid sequence encoding a reporter operably linked to a rat promoter sequence, with an agent and detecting the expression of a product of the nucleic acid sequence encoding the reporter in the test cell.
8. The method of claim 7 wherein a decrease in the expression of a product of the nucleic acid sequence encoding the reporter in the test cell contacted with the

agent relative to the expression of the product of the nucleic acid sequence encoding the reporter in a test cell not contacted with the agent, indicates that the agent causes a decrease in expression of a product of the nucleic acid sequence encoding Rat in the test cell.

9. The method of claim 7 wherein an increase in the expression of a product of the nucleic acid sequence encoding the reporter in the test cell contacted with the agent relative to the expression of the product of the nucleic acid sequence encoding the reporter in a test cell not contacted with the agent, indicates that the agent causes an increase in expression of a product of the nucleic acid sequence encoding Rat in the test cell.

10. The method of claim 7 wherein the bacterium is Staphylococcus aureus.

11. The method of claim 7 wherein the bacterium comprises Staphylococcus, Sinorhizobium, Listeria, Clostridium, Bacillus, Corynebacterium, Brucella, Pseudomonas, Shweanella, Mesorhizobium, Caulobacter, Lactococcus, Mycobacterium, Burkholderia, Geobacter, Treponema, Vibrio, Escherichia, Enterococcus, Salmonella, Klebsiella, Agrobacterium, Yersinia, Bordetella, Actinobacillus, Streptomyces, Streptococcus, or Acinetobacter.

12. A method of inhibiting growth and infectivity of a bacterium comprising contacting the bacteria with an agent identified by the method of claim 7.

13. The method of claim 12 further comprising an antibiotic.

14. The method of claim 12 wherein the bacterium is Staphylococcus aureus.

15. The method of claim 12 where the bacterium comprises Staphylococcus, Sinorhizobium, Listeria, Clostridium, Bacillus, Corynebacterium, Brucella, Pseudomonas, Shweanella, Mesorhizobium, Caulobacter, Lactococcus, Mycobacterium, Burkholderia, Geobacter, Treponema, Vibrio, Escherichia, Enterococcus, Salmonella, Klebsiella, Agrobacterium, Yersinia, Bordetella, Actinobacillus, Streptomyces, Streptococcus, or Acinetobacter.

16. A pharmaceutical composition for use as an anti-bacterial agent comprising an agent identified by the method of claim 7 and a pharmaceutically acceptable vehicle.

17. The pharmaceutical composition of claim 16 further comprising an antibiotic.

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File: DWPI

Sep 6, 2002

DERWENT-ACC-NO: 2002-706985
DERWENT-WEEK: 200276
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TITLE: New sarR gene from the locus of Staphylococcus aureus, useful for treating gram-positive bacteremia

INVENTOR: CHEUNG, A L; MANNA, A ; ZHANG, G

PRIORITY-DATA: 2001US-289601P (May 8, 2001), 2001US-261233P (January 12, 2001),
2001US-261607P (January 12, 2001)

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PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<input type="checkbox"/> <u>WO 200268610 A2</u>	September 6, 2002	E	062	C12N000/00

INT-CL (IPC): C12 N 0/00

ABSTRACTED-PUB-NO: WO 200268610A
BASIC-ABSTRACT:

NOVELTY - An isolated nucleic acid sequence (I), which regulates the expression of virulence determinants in gram-positive bacteria, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

- (1) a vector (II) comprising the nucleic acid sequence;
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- (6) an isolated polypeptide (VII) that regulates the expression of virulence determinants in gram-positive bacteria;
- (7) a kit (VIII) for identifying the presence of a sarR gene or its product comprising a means for analyzing a biological sample for the presence of the sarR gene or its product;

(8) a method (IX) of treating a mammal suffering from or susceptible to a gram-positive bacterial infection; or

(9) a method (X) of screening for lead compounds that inhibit the expression of virulence determinants in gram-positive bacteria.

ACTIVITY - Antibacterial.

No biological data given.

MECHANISM OF ACTION - SarR-Agonist.

USE - The pharmaceutical composition comprising a sarR agonist or a compound capable of selective occupation of a sarA promoter receptor is useful for treating gram-positive bacteremia (claimed).

ABSTRACTED-PUB-NO: WO 200268610A

EQUIVALENT-ABSTRACTS:

CHOSEN-DRAWING: Dwg.0/12

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DESIGNATED-STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE
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APPLICATION-DATA:

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
WO 200268610A2	January 11, 2002	2002WO-US00877	

INT-CL (IPC): C12 N 0/00

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infectivity of bacteria;

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DERWENT-CLASS: B04 D16

CPI-CODES: B04-C01; B04-E01; B04-E02F; B04-E03F; B04-E08; B04-F0100E; B04-F10B; B04-F10B0E; B04-F10B3; B04-F10B3E; B04-N03A0E; B11-A01; B11-C08E1; B11-C08F; B11-C08F2; B11-C08F4; B11-C08G; B11-C10; B12-K04E; B14-A01B; B14-A01B4; D05-H04; D05-H08; D05-H09; D05-H12A; D05-H12E; D05-H14; D05-H17A6; D05-H18;

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L3: Entry 5 of 6

File: DWPI

Sep 6, 2002

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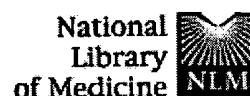
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- ☐ 1: [Cheung AL, Bayer AS, Zhang G, Gresham H, Xiong YQ.](#) Related Articles, Links



Regulation of virulence determinants in vitro and in vivo in *Staphylococcus aureus*.

FEMS Immunol Med Microbiol. 2004 Jan 15;40(1):1-9. Review.
PMID: 14734180 [PubMed - indexed for MEDLINE]

PubMed Services

- ☐ 2: [Schmidt KA, Manna AC, Cheung AL.](#) Related Articles, Links



SarT influences sarS expression in *Staphylococcus aureus*.

Infect Immun. 2003 Sep;71(9):5139-48.
PMID: 12933857 [PubMed - indexed for MEDLINE]

Related Resources

- ☐ 3: [Kupferwasser LI, Yeaman MR, Nast CC, Kupferwasser D, Xiong YQ, Palma M, Cheung AL, Bayer AS.](#) Related Articles, Links



Salicylic acid attenuates virulence in endovascular infections by targeting global regulatory pathways in *Staphylococcus aureus*.

J Clin Invest. 2003 Jul;112(2):222-33.
PMID: 12865410 [PubMed - indexed for MEDLINE]

- ☐ 4: [Li R, Manna AC, Dai S, Cheung AL, Zhang G.](#) Related Articles, Links



Crystal structure of the SarS protein from *Staphylococcus aureus*.

J Bacteriol. 2003 Jul;185(14):4219-25.
PMID: 12837797 [PubMed - indexed for MEDLINE]

- ☐ 5: [Manna AC, Cheung AL.](#) Related Articles, Links



sarU, a sarA homolog, is repressed by SarT and regulates virulence genes in *Staphylococcus aureus*.

Infect Immun. 2003 Jan;71(1):343-53.
PMID: 12496184 [PubMed - indexed for MEDLINE]

- ☐ 6: [van Wamel W, Xiong YQ, Bayer AS, Yeaman MR, Nast CC, Cheung AL.](#) Related Articles, Links



Regulation of *Staphylococcus aureus* type 5 capsular polysaccharides by agr and sarA in vitro and in an experimental endocarditis model.

Microb Pathog. 2002 Aug;33(2):73-9.
PMID: 12202106 [PubMed - indexed for MEDLINE]

- ☐ 7: Heyer G, Saba S, Adamo R, Rush W, Soong G, Cheung A, Prince A. Related Articles, Links



Staphylococcus aureus agr and sarA functions are required for invasive infection but not inflammatory responses in the lung.
Infect Immun. 2002 Jan;70(1):127-33.
PMID: 11748173 [PubMed - indexed for MEDLINE]

- ☐ 8: Cheung AL, Zhang G. Related Articles, Links



Are the structures of SarA and SarR similar?
Trends Microbiol. 2001 Dec;9(12):570-3. No abstract available.
PMID: 11728861 [PubMed - indexed for MEDLINE]

- ☒ 9: Palma M, Cheung AL. Related Articles, Links



sigma(B) activity in Staphylococcus aureus is controlled by RsbU and an additional factor(s) during bacterial growth.
Infect Immun. 2001 Dec;69(12):7858-65.
PMID: 11705968 [PubMed - indexed for MEDLINE]

- ☐ 10: Kielian T, Cheung A, Hickey WF. Related Articles, Links



Diminished virulence of an alpha-toxin mutant of Staphylococcus aureus in experimental brain abscesses.
Infect Immun. 2001 Nov;69(11):6902-11.
PMID: 11598065 [PubMed - indexed for MEDLINE]

- ☒ 11: Schmidt KA, Manna AC, Gill S, Cheung AL. Related Articles, Links



SarT, a repressor of alpha-hemolysin in Staphylococcus aureus.
Infect Immun. 2001 Aug;69(8):4749-58.
PMID: 11447147 [PubMed - indexed for MEDLINE]

- ☒ 12: Liu Y, Manna A, Li R, Martin WE, Murphy RC, Cheung AL, Zhang G. Related Articles, Links



Crystal structure of the SarR protein from Staphylococcus aureus.
Proc Natl Acad Sci U S A. 2001 Jun 5;98(12):6877-82. Epub 2001 May 29.
PMID: 11381122 [PubMed - indexed for MEDLINE]

- ☐ 13: Cheung AL, Schmidt K, Bateman B, Manna AC. Related Articles, Links



SarS, a SarA homolog repressible by agr, is an activator of protein A synthesis in Staphylococcus aureus.
Infect Immun. 2001 Apr;69(4):2448-55.
PMID: 11254606 [PubMed - indexed for MEDLINE]

- ☒ 14: Manna A, Cheung AL. Related Articles, Links



Characterization of sarR, a modulator of sar expression in Staphylococcus aureus.
Infect Immun. 2001 Feb;69(2):885-96.
PMID: 11159982 [PubMed - indexed for MEDLINE]

☐ **15:** [Chien Y, Manna AC, Projan SJ, Cheung AL.](#) [Related Articles](#), [Links](#)



SarA, a global regulator of virulence determinants in *Staphylococcus aureus*, binds to a conserved motif essential for sar-dependent gene regulation.

J Biol Chem. 1999 Dec 24;274(52):37169-76.

PMID: 10601279 [PubMed - indexed for MEDLINE]

☐ **16:** [Cheung AL, Chien YT, Bayer AS.](#) [Related Articles](#), [Links](#)



Hyperproduction of alpha-hemolysin in a sigB mutant is associated with elevated SarA expression in *Staphylococcus aureus*.

Infect Immun. 1999 Mar;67(3):1331-7.

PMID: 10024579 [PubMed - indexed for MEDLINE]

☐ **17:** [Manna AC, Bayer MG, Cheung AL.](#) [Related Articles](#), [Links](#)



Transcriptional analysis of different promoters in the sar locus in *Staphylococcus aureus*.

J Bacteriol. 1998 Aug;180(15):3828-36.

PMID: 9683479 [PubMed - indexed for MEDLINE]

☐ **18:** [Fluckiger U, Wolz C, Cheung AL.](#) [Related Articles](#), [Links](#)



Characterization of a sar homolog of *Staphylococcus epidermidis*.

Infect Immun. 1998 Jun;66(6):2871-8.

PMID: 9596762 [PubMed - indexed for MEDLINE]

☐ **19:** [Chien Y, Cheung AL.](#) [Related Articles](#), [Links](#)



Molecular interactions between two global regulators, sar and agr, in *Staphylococcus aureus*.

J Biol Chem. 1998 Jan 30;273(5):2645-52.

PMID: 9446568 [PubMed - indexed for MEDLINE]

☐ **20:** [Cheung AL, Eberhardt K, Heinrichs JH.](#) [Related Articles](#), [Links](#)



Regulation of protein A synthesis by the sar and agr loci of *Staphylococcus aureus*.

Infect Immun. 1997 Jun;65(6):2243-9.

PMID: 9169758 [PubMed - indexed for MEDLINE]

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| www.pnas.org/cgi/content/abstract/94/22/12088 [Save](#)

IOVS -- Ruan et al. 43 (5): 1414

0 kg) were injected intrastromally with approximately 100 colony-
forming units of log phase S. aureus (**RN6390**, a wild-type strain
generously...

www.iovs.org/cgi/content/full/43/5/1414 [Save](#)

IOVS -- Giese et al. 41 (1): 145

...and Components In this study, a wild-type (WT) strain (**RN6390**) of
S. aureus was used in the in vivo experiments. **RN6390** is a
laboratory...

www.iovs.org/cgi/content/full/41/1/145 [Save](#)

Circulation -- Kupferwasser et al. 99 (21): 2791

Aggregation data for S aureus ISP 479C were virtually identical to
those seen with strains ISP479R, **RN6390**, 6850, and 8325-4 (data
not shown).

| circ.ahajournals.org/cgi/content/full/99/21/2791 [Save](#)

Goulian

"Staphylococcus aureus **RN6390** Replicates and Induces Apoptosis in
a Pulmonary Epithelial Cell Line", B.C. Kahl, M. Goulian, W. Van
Wamel, M....

| dept.physics.upenn.edu/facultyinfo/goulian.html [Save](#)

MMBR -- Abstracts: Finlay and Falkow 61 (2): 136

Herrmann, M., Simon, S. M., Kaplan, G., Peters, G., Cheung, A. L.
(2000). Staphylococcus aureus **RN6390** Replicates and Induces

Apoptosis in a...

 | mimbr.asm.org/cgi/content/abstract/61/2/136 [Save](#)

[Microbiology -- Garvis et al. 148 \(10\): 3235](#)

Chromosomal DNA from *S. aureus* **RN6390** was isolated as described by Pospiech & Neumann (1995) . DNA restriction and modifications were...

mic.sgmjournals.org/cgi/content/full/148/10/3235 [Save](#)

1 2 3 4 5 6 7 Next »

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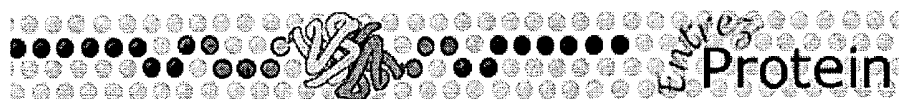
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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for Limits ☐ 1: AAA62477. staphylococcal ac...[gi:684950]

BLink, Domains, Links

LOCUS AAA62477 124 aa linear BCT 28-OCT-1994

DEFINITION staphylococcal accessory regulator A.

ACCESSION AAA62477

VERSION AAA62477.1 GI:684950

DBSOURCE locus SAU20782 accession U20782.1

KEYWORDS .

SOURCE Staphylococcus aureus

ORGANISM Staphylococcus aureus

Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (residues 1 to 124)

AUTHORS Cheung,A.L. and Projan,S.J.

TITLE Cloning and sequencing of sarA of Staphylococcus aureus, a gene required for the expression of agr

JOURNAL J. Bacteriol. 176 (13), 4168-4172 (1994)

MEDLINE 94292439

PUBMED 8021198

REFERENCE 2 (residues 1 to 124)

AUTHORS Cheung,A.L., Koomey,J.M., Butler,C.A., Projan,S.J. and

Fischetti,V.A.

TITLE Regulation of exoprotein expression in Staphylococcus aureus by a locus (sar) distinct from agr

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6462-6466 (1992)

MEDLINE 92335318

PUBMED 1321441

REFERENCE 3 (residues 1 to 124)

AUTHORS Cheung,A.L.

TITLE Direct Submission

JOURNAL Submitted (08-FEB-1995) Ambrose L. Cheung, Rockefeller University, Bacterial Pathogenesis and Immunology, 1230 York Avenue, New York, NY 10021, USA

COMMENT On Feb 28, 1995 this sequence version replaced gi:560643.

Method: conceptual translation.

FEATURES Location/Qualifiers

source

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/organism="Staphylococcus aureus"

/strain="RN450"

/db_xref="taxon:1280"

/map="SmaI D fragment"

Protein

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/function="regulator of exoprotein expression; regulator of agr expression"

CDS

1..124

/gene="sarA"


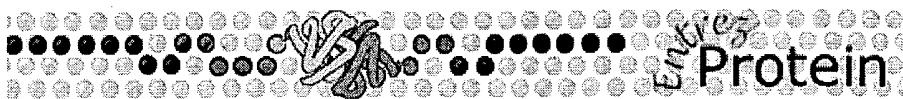
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h cb hg e e e e fcg b e

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: AAA62477. staphylococcal ac...[gi:684950] BLink, Domains, Links

LOCUS AAA62477 124 aa linear BCT 28-OCT-1994

DEFINITION staphylococcal accessory regulator A.

ACCESSION AAA62477

VERSION AAA62477.1 GI:684950

DBSOURCE locus SAU20782 accession [U20782.1](#)

KEYWORDS .

SOURCE Staphylococcus aureus

ORGANISM Staphylococcus aureus

Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (residues 1 to 124)

AUTHORS Cheung,A.L. and Projan,S.J.

TITLE Cloning and sequencing of sarA of Staphylococcus aureus, a gene required for the expression of agr

JOURNAL J. Bacteriol. 176 (13), 4168-4172 (1994)

MEDLINE [94292439](#)

PUBMED [8021198](#)

REFERENCE 2 (residues 1 to 124)

AUTHORS Cheung,A.L., Koomey,J.M., Butler,C.A., Projan,S.J. and

Fischetti,V.A.

TITLE Regulation of exoprotein expression in Staphylococcus aureus by a locus (sar) distinct from agr

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6462-6466 (1992)

MEDLINE [92335318](#)

PUBMED [1321441](#)

REFERENCE 3 (residues 1 to 124)

AUTHORS Cheung,A.L.

TITLE Direct Submission

JOURNAL Submitted (08-FEB-1995) Ambrose L. Cheung, Rockefeller University, Bacterial Pathogenesis and Immunology, 1230 York Avenue, New York, NY 10021, USA

COMMENT On Feb 28, 1995 this sequence version replaced gi:[560643](#).

Method: conceptual translation.

FEATURES Location/Qualifiers

source

1..124

/organism="Staphylococcus aureus"

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/db_xref="taxon:1280"

/map="SmaI D fragment"

Protein

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/product="staphylococcal accessory regulator A"

/function="regulator of exoprotein expression; regulator of agr expression"

CDS

1..124

/gene="sarA"



/coded_by="U20782.1:19..393"

/transl_table=11

ORIGIN

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61 nykqpqvka vkilsqedyf dkkrnehder tvlilvnaqq rkkiesllsr vnkriteann

h cb hg e e e e fcg b e

  **Protein**

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: AAB05395. ORF3...[gi:1477532] BLink, Links

LOCUS AAB05395 39 aa linear BCT 02-AUG-1996

DEFINITION ORF3.

ACCESSION AAB05395

VERSION AAB05395.1 GI:1477532

DBSOURCE locus SAU46541 accession [U46541.1](#)

KEYWORDS .

SOURCE Staphylococcus aureus

ORGANISM [Staphylococcus aureus](#)

Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (residues 1 to 39)

AUTHORS Bayer, M.G., Heinrichs, J.H. and Cheung, A.L.

TITLE The molecular architecture of the sar locus in Staphylococcus aureus

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 39)

AUTHORS Cheung, A.L. and Projan, S.J.

TITLE Cloning and sequencing of sarA of Staphylococcus aureus, a gene required for the expression of agr

JOURNAL J. Bacteriol. 176 (13), 4168-4172 (1994)

MEDLINE [94292439](#)

PUBMED [8021198](#)

REFERENCE 3 (residues 1 to 39)

AUTHORS Cheung, A.L.

TITLE Direct Submission

JOURNAL Submitted (18-JAN-1996) Ambrose L. Cheung, Bacterial Pathogenesis & Immunology, Rockefeller University, 1230 York Avenue, New York, NY 10021, USA

COMMENT Method: conceptual translation.

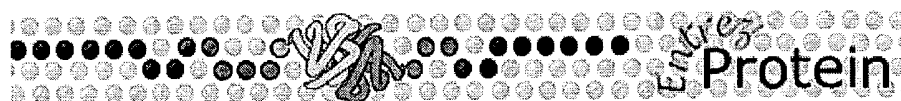
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/strain="RN6390"
/db_xref="taxon:1280"
Protein 1..39
/function="unknown"
/name="ORF3"
CDS 1..39
/coded_by="U46541.1:599..718"
/transl_table=11

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1 mlifltkpna npeiqlclm nnlfykhffv yfsflisyn

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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for

Limits Preview/Index History Clipboard Details
 Show:

☐ 1: AAB05396. sarA...[gi:1477533]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAB05396 113 aa linear BCT 02-AUG-1996

DEFINITION sarA.

ACCESSION AAB05396

VERSION AAB05396.1 GI:1477533

DBSOURCE locus SAU46541 accession [U46541.1](#)

KEYWORDS .

SOURCE Staphylococcus aureus

ORGANISM [Staphylococcus aureus](#)

Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (residues 1 to 113)

AUTHORS Bayer, M.G., Heinrichs, J.H. and Cheung, A.L.

TITLE The molecular architecture of the sar locus in Staphylococcus aureus

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 113)

AUTHORS Cheung, A.L. and Projan, S.J.

TITLE Cloning and sequencing of sarA of Staphylococcus aureus, a gene required for the expression of agr

JOURNAL J. Bacteriol. 176 (13), 4168-4172 (1994)

MEDLINE [94292439](#)

PUBMED [8021198](#)

REFERENCE 3 (residues 1 to 113)

AUTHORS Cheung, A.L.

TITLE Direct Submission

JOURNAL Submitted (18-JAN-1996) Ambrose L. Cheung, Bacterial Pathogenesis & Immunology, Rockefeller University, 1230 York Avenue, New York, NY 10021, USA

COMMENT Method: conceptual translation.

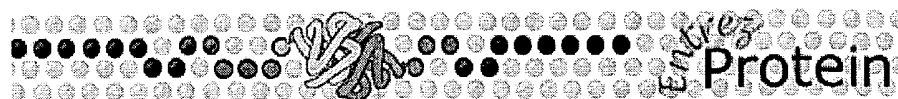
FEATURES Location/Qualifiers

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 /strain="RN6390"
 /db_xref="taxon:1280"
 Protein 1..113
 /product="sarA"
 /function="regulatory gene"
 CDS 1..113
 /gene="sarA"
 /coded_by="U46541.1:866..1207"
 /transl_table=11

ORIGIN

1 maitkindcf ellsmvtyad klkslikkef sisfeefavl tyisenkeke yyfkdiinh1
 61 nykqpqvka vkilsqedyf dkkrnehder tvlilvnaqq rkkiesllsr vnk

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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for

Limits Preview/Index History Clipboard Details
 Show:

☐ 1: AAC25106. staphylococcal ac...[gi:3283053]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAC25106 124 aa linear BCT 02-JUL-1998

DEFINITION staphylococcal accessory regulator A homolog [Staphylococcus epidermidis].

ACCESSION AAC25106

VERSION AAC25106.1 GI:3283053

DBSOURCE locus AF054173 accession [AF054173.1](#)

KEYWORDS .

SOURCE Staphylococcus epidermidis

ORGANISM Staphylococcus epidermidis

Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (residues 1 to 124)

AUTHORS Fluckiger,U., Wolz,C. and Cheung,A.L.

TITLE Characterization of a sar homolog of Staphylococcus epidermidis

JOURNAL Infect. Immun. (1998) In press

REFERENCE 2 (residues 1 to 124)

AUTHORS Cheung,A.L.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1998) Bacterial Pathogenesis & Immunology, Rockfeller University, 1230 York Avenue, New York, NY 10021, USA

COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..124
 /organism="Staphylococcus epidermidis"
 /isolate="6937"
 /db_xref="taxon:1282"

Protein 1..124
 /product="staphylococcal accessory regulator A homolog"

CDS 1..124
 /gene="sarA"
 /coded_by="AF054173.1:887..1261"
 /transl_table=11

ORIGIN

1 maiskindcf ellamvtyad rlkgiikkef sisfeefavl tyisenkeee yylkdiinh1.
 61 nykqpqvka vknlsqenyf nkkrnehder tvlilvdskq rkkiddllkr vnnriteann
 121 enev

//

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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

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Display Limits Preview/Index History Clipboard Details

☐ 1: AAG35715. SarR [Staphylococ...[gi:11493942]

BLink, Links

LOCUS AAG35715 115 aa linear BCT 01-DEC-2000

DEFINITION SarR [Staphylococcus aureus].

ACCESSION AAG35715

VERSION AAG35715.1 GI:11493942

DBSOURCE locus AF207701 accession AF207701.1

KEYWORDS .

SOURCE Staphylococcus aureus

ORGANISM Staphylococcus aureus

Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (residues 1 to 115)

AUTHORS Cheung,A.L. and Manna,A.C.

TITLE Characterization of sarR, a modulator of sar expression in Staphylococcus aureus

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 115)

AUTHORS Cheung,A.L. and Manna,A.C.

TITLE Direct Submission

JOURNAL Submitted (22-NOV-1999) Microbiology, Dartmouth Medical School, College St, Vail 206, Hanover, NH 03755, USA

COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..115
 /organism="Staphylococcus aureus"
 /strain="RN6390"
 /db_xref="taxon:1280"

Protein 1..115
 /product="SarR"
 /note="similar to SarA"

CDS 1..115
 /gene="sarR"
 /coded_by="AF207701.1:208..555"
 /transl_table=11

ORIGIN


1 mskindindl vnatfqvkkf frdtkkkfnl nyeeiyilnh ilrsesneis skeiakcsef
 61 kpyyltkalq klkdlklslk krsldqertv ivyvttdtqka niqklisele eyikn

//

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Entry information

Entry name	Q9F0R1
Primary accession number	Q9F0R1
Secondary accession numbers	None
Entered in TrEMBL in	Release 16, March 2001
Sequence was last modified in	Release 16, March 2001
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	SarR
Synonym	Staphylococcal accessory regulator A homolog
Gene name	SARR or SAV2295 or SA2089 or MW2213
From	Staphylococcus aureus (strain Mu50 / ATCC 700699) [TaxID: 158878] Staphylococcus aureus (strain N315) [TaxID: 158879] Staphylococcus aureus [TaxID: 1280] Staphylococcus aureus (strain MW2) [TaxID: 196620]
Taxonomy	Bacteria; Firmicutes; Bacillales; Staphylococcus.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=RN6390;
Cheung A.L., Manna A.C.;
 "Characterization of sarR, a modulator of sar expression in Staphylococcus aureus.";
 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=Mu50, and N315;
 MEDLINE=21311952; PubMed=11418146; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
 Lancet 357:1225-1240(2001).
- [3] SEQUENCE FROM NUCLEIC ACID.
STRAIN=MW2;
 MEDLINE=22040717; PubMed=12044378; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
 "Genome and virulence determinants of high virulence community-acquired MRSA.";
 Lancet 359:1819-1827(2002).

Comments

None

Cross-references

EMBL	AF207701; AAG35715.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP003364; BAB58457.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP003136; BAB43387.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP004829; BAB96078.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	B90028; B90028.
CMR	Q9F0R1; SAV2295.
InterPro	IPR010166 ; Staph_reg_Sar. IPR009058 ; Wing_hlx_DNA_bnd. Graphical view of domain structure.
TIGRFAMs	TIGR01889 ; Staph_reg_Sar; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q9F0R1 .
PRESAGE	Q9F0R1 .
ModBase	Q9F0R1 .
SMR	Q9F0R1 ; D2CE40E2DB234DBD.
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Complete proteome

Features

None

Sequence information

Length: 115 AA Molecular weight: 13669 Da CRC64: D2CE40E2DB234DBD [This is a checksum on the sequence]

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70	80	90	100	110	
KPYYLTKALQ	KLKDLKLLSK	KRSLQDERTV	IVYVTDTOKA	NIQKLISELE	EYIKN

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or at [NCBI \(USA\)](#)



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[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet](#) (Java)



[ScanProsite](#), [MotifScan](#)




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Entry information

Entry name	Q8CNC4
Primary accession number	Q8CNC4
Secondary accession numbers	None
Entered in TrEMBL in	Release 23, March 2003
Sequence was last modified in	Release 23, March 2003
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	SarR protein
Synonyms	None
Gene name	<u>SE1868</u>
From	<u>Staphylococcus epidermidis</u> [TaxID: 1282]
Taxonomy	<u>Bacteria</u> ; <u>Firmicutes</u> ; <u>Bacillales</u> ; <u>Staphylococcus</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y.;
 Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AE016750; AAO05509.1; - [EMBL / GenBank / DDBJ] [CoDingSequence]
CMR	Q8CNC4; SE1868.
InterPro	IPR010166; Staph_reg_Sar. IPR009058; Wing_hlx_DNA_bnd. Graphical view of domain structure.
TIGRFAMs	TIGR01889; Staph_reg_Sar; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q8CNC4.
PRESAGE	Q8CNC4.
ModBase	Q8CNC4.
SMR	Q8CNC4; A401B6F9FE6BBCAB.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Complete proteome.

Features

None

Sequence information

Length: 114 AA	Molecular weight: 13590 Da	CRC64: A401B6F9FE6BBCAB [This is a checksum on the sequence]				
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70	80	90	100	110		
KPYLYTKALQ	KLKDLNLLSK	KRSVHDERTV	IVFVSDEQRE	KIKKLILELE	NYIK	

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[BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet](#) (Java)




[ScanProsite](#), [MotifScan](#)



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Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Canada	China	Korea	Switzerland	Taiwan
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TrEMBL:

Q53776

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	Q53776
Primary accession number	Q53776
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 19, December 2001

Name and origin of the protein

Protein name	SarA
Synonyms	None
Gene name	None
From	<u>Staphylococcus aureus</u> [TaxID: 1280]
Taxonomy	Bacteria; Firmicutes; Bacillales; Staphylococcus.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=RN6390;
Bayer M.G., Heinrichs J.H., Cheung A.L.;
"The molecular architecture of the sar locus in Staphylococcus aureus.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=RN6390;
MEDLINE=94292439; **PubMed**=8021198; [NCBI, ExPASy, EBI, Israel, Japan]
Cheung A.L., Projan S.J.;
"Cloning and sequencing of sarA of Staphylococcus aureus, a gene required for the expression of agr.";
J. Bacteriol. 176:4168-4172(1994).

Comments

None

Cross-references

EMBL	U46541; AAB05395.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q53776 .
PRESAGE	Q53776 .
ModBase	Q53776 .
SMR	Q53776 ; C5F205826F21D35B.
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features

None

Sequence information

Length: 39 AA	Molecular weight: 4723 Da	CRC64: C5F205826F21D35B [This is a checksum on the sequence]
<div> <div>10</div> <div>20</div> <div>30</div> </div> <div> MLIFLTKPNA NPEIQSLCLM NNLFYKHFFV YFSFLISYN </div>		
Q53776 in FASTA format		

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 or at [NCBI \(USA\)](#)



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[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet](#) (Java)



[ScanProsite](#), [MotifScan](#)




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Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan				
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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name	Q53600
Primary accession number	Q53600
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	Staphylococcal accessory regulator variant	
Synonym	Staphylococcal accessory regulator A	
Gene name	SARA or SAV0616 or SA0573 or MW0580	
From	Staphylococcus aureus	[TaxID: 1280]
	Staphylococcus aureus (strain Mu50 / ATCC 700699)	[TaxID: 158878]
	Staphylococcus aureus (strain N315)	[TaxID: 158879]
	Staphylococcus aureus (strain MW2)	[TaxID: 196620]
Taxonomy	Bacteria; Firmicutes; Bacillales; Staphylococcus.	

References

- [1] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*S.aureus*;
Shawcross S.G., Edwards-Jones V., Dawson M.M., Foster H.A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*S.aureus*;
STRAIN=RN450;
MEDLINE=94292439; PubMed=8021198; [NCBI, ExPASy, EBI, Israel, Japan]
Cheung A.L., Projan S.J.;
"Cloning and sequencing of *sarA* of *Staphylococcus aureus*, a gene required for the expression of *agr*.";
J. Bacteriol. 176:4168-4172(1994).
- [3] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*S.aureus*;
STRAIN=RN450;
MEDLINE=92335318; PubMed=1321441; [NCBI, ExPASy, EBI, Israel, Japan]
Cheung A.L., Koomey J.M., Butler C.A., Projan S.J., Fischetti V.A.;
"Regulation of exoprotein expression in *Staphylococcus aureus* by a locus (*sar*) distinct from *agr*.";
Proc. Natl. Acad. Sci. U.S.A. 89:6462-6466(1992).
- [4] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*S.aureus*;
STRAIN=RN450;
Cheung A.L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
- [5] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*S.aureus*;
STRAIN=Mu50, and N315;
MEDLINE=21311952; PubMed=11418146; [NCBI, ExPASy, EBI, Israel, Japan]
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I.,
Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H.,
Kuhara S., Goto S., Yabuzaki J., Kanchisa M., Yamashita A., Oshima K., Furuya K., Yoshino C.,
Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.";
Lancet 357:1225-1240(2001).
- [6] SEQUENCE FROM NUCLEIC ACID.
SPECIES=*S.aureus*;
STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378; [NCBI, ExPASy, EBI, Israel, Japan]
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K.,
Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-acquired MRSA."; *Lancet* 359:1819-1827(2002).

Comments

None

Cross-references

EMBL	AF515775; AAM74164.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] U20782; AAA62477.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP003359; BAB56778.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP003131; BAB41805.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP004824; BAB94445.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	B89831; B89831.
CMR	Q53600; SAV0616.
InterPro	IPR010166 ; Staph_reg_Sar. IPR009058 ; Wing_hlx_DNA_bnd. Graphical view of domain structure.
TIGRFAMs	TIGR01889; Staph_reg_Sar; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q53600 .
PRESAGE	Q53600 .
ModBase	Q53600 .
SMR	Q53600 ; DB9A16E806C10661.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords**[Complete proteome.](#)****Features**

None


Sequence information

Length: 124 AA Molecular weight: 14718 Da CRC64: DB9A16E806C10661 [This is a checksum on the sequence]

10	20	30	40	50	60
MAITKINDCF	ELLSMVTYAD	KLKSLIKKEF	SISFEFAVL	TYISENKEKE	YYLKDIINHL
70	80	90	100	110	120
NYKQPQVVKA	VKILSQEDYF	DKKRNEHDER	TVLILVNAQQ	RKKIESLLSR	VNKRITEANN

EIEL

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[\[Features\]](#)
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[\[Tools\]](#)

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Entry information

Entry name	O85233
Primary accession number	O85233
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	Staphylococcal accessory regulator A homolog
Synonyms	None
Gene name	SARA or SE0390
From	Staphylococcus epidermidis [TaxID: 1282]
Taxonomy	Bacteria; Firmicutes ; Bacillales ; Staphylococcus .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=6937;
[Fluckiger U.](#), [Wolz C.](#), [Cheung A.L.](#);
"Characterization of a sar homolog of Staphylococcus epidermidis."
[Infect. Immun.](#) 0:0-0(1998).
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 12228;
[Zhang Y.](#), [Ren S.](#), [Li H.](#), [Fu G.](#), [Lu L.](#), [Lu G.](#), [Jia J.](#), [Tu Y.](#), [Qin Z.](#), [Chen Z.](#), [Wen Y.](#);
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AF054173 ; AAC25106.1 ; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE016745 ; AAO03987.1 ; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
CMR	O85233 ; SE0390 .
InterPro	IPR010166 ; Staph_reg_Sar . IPR009058 ; Wing_hlx_DNA_bnd . Graphical view of domain structure .
TIGRFAMs	TIGR01889 ; Staph_reg_Sar ; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	O85233 .
PRESAGE	O85233 .
ModBase	O85233 .
SMR	O85233 ; 4D1D10E47D574266 .
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least 50% / 90% identity .

Keywords**Complete proteome.****Features**

None

Sequence information

Length: 124 AA	Molecular weight: 14731 Da	CRC64: 4D1D10E47D574266 [This is a checksum on the sequence]			
10	20	30	40	50	60
MAISKINDCF	ELLAMVTYAD	RLKGIKKEF	SISFEFAVL	TYISENKEEE	YYLKDIINHL
70	80	90	100	110	120
NYKQPQVVKA	VKNLSQENYF	NKKRNEHDER	TVLILVDSKQ	RKKIDDLLKR	VNNRITEANN
ENEV					
O85233 in FASTA format					

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